version of Nle was generated by introducing three copies of the HA epitope (YPUDVPDYA) (SEQ ID NO: 8) immediately downstream of the first Methionine residue. The *Bam*HI-*Asc*I fragment of pKS-Nle was replaced by a corresponding PCR fragment amplified using the following primers:

A1 Cur

5' CGGATCCAAA AAATGTATCC CTATGACGTC CCCGATTATG CCTACCCTTA CGATGTACCT GACTACGCGT ATCCGTACGA CGTTCCGGAC TATGCTCAGG AGACGGACA CGGAGCAAGA GGCCACGCCA CATACGATAC AGGCGCGCCA A 3' (SEQ ID NO: 9), and

5' TAAACGAGGC GCGCCTATCG TAT 3' (SEQ ID NO: 10).--

Please replace the paragraph at page 22, lines 18-22 with the following rewritten paragraph:

--*XNle* was isolated by PCR using the degenerate primers, F 5'-CGC AGA ATT CCI TTY GAY GTI CCI GTI GAY AT-3' (SEQ ID NO: 11) and R 5'-GGT GCT CGA GCY TGI GGY TGR TAI ATD ATR TC-3' (SEQ ID NO: 12), designed against conserved peptides, PFDVPVDI (SEQ ID NO: 13) and DIIYQPQ (SEQ ID NO: 14) respectively, found in the Nle domain of the vertebrate proteins identified as expressed sequence tags.--

A2

Please replace the paragraph at page 22, line 23 to page 23, line 2 with the following rewritten paragraph:

--Phage stock of a stage 30 library (Stratagene) was used as template to amplify a 200bp fragment that spans Nle domain. Five independent clones were sequenced and found to be identical. This fragment was used to screen the stage 30 library, which resulted in the isolation of 25 positive clones of which the longest of 2.2Kb was sequenced on both strands. Temporal expression was assayed by RT-PCR analysis as

A3